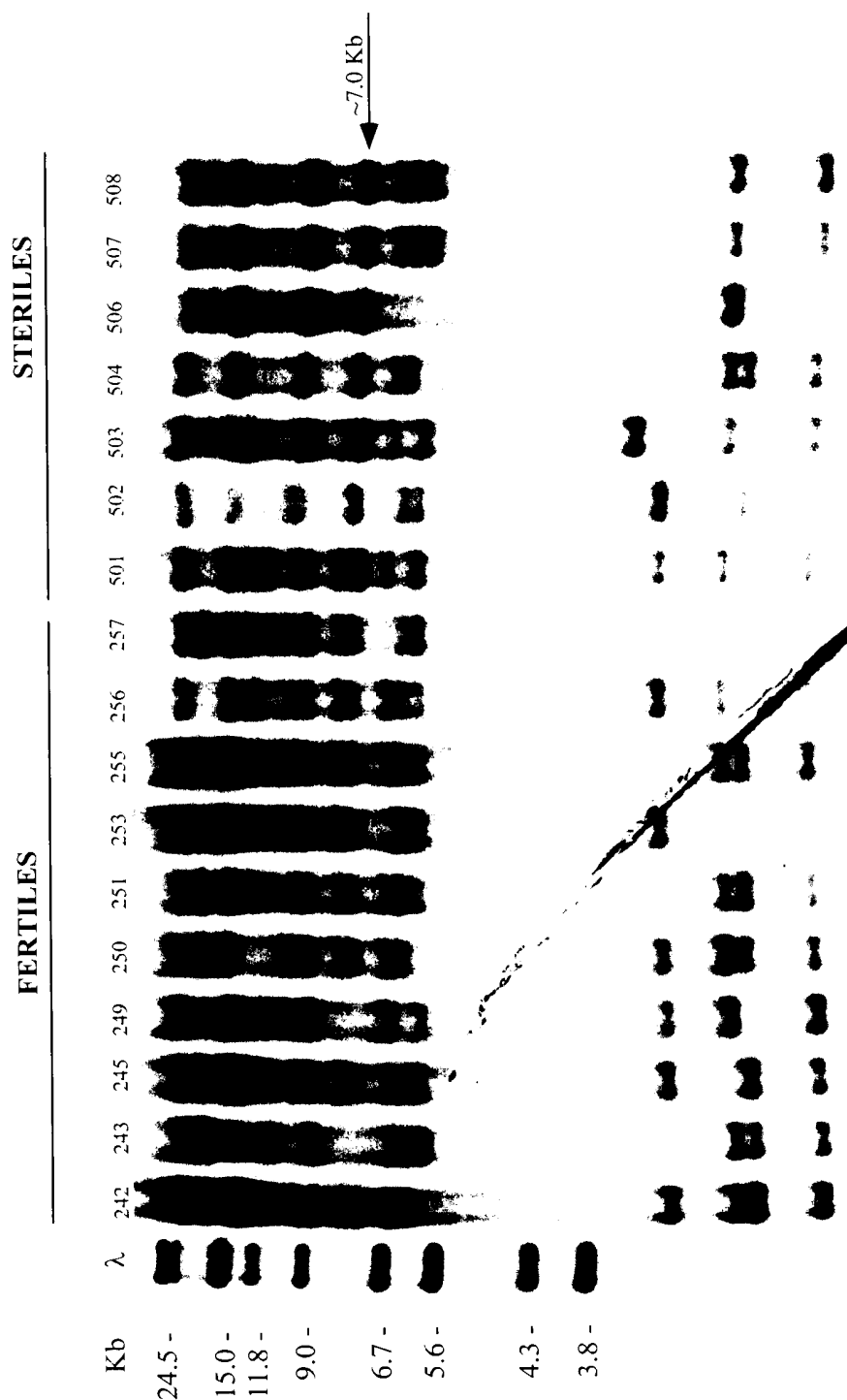


FIGURE 1



SOUTHERN OF ECORI DIGESTED DNA FROM THE MALE STERILE FAMILY BS92-7. HYBRIDIZED WITH THE MU1 TRANSPOSON.

Figure 2

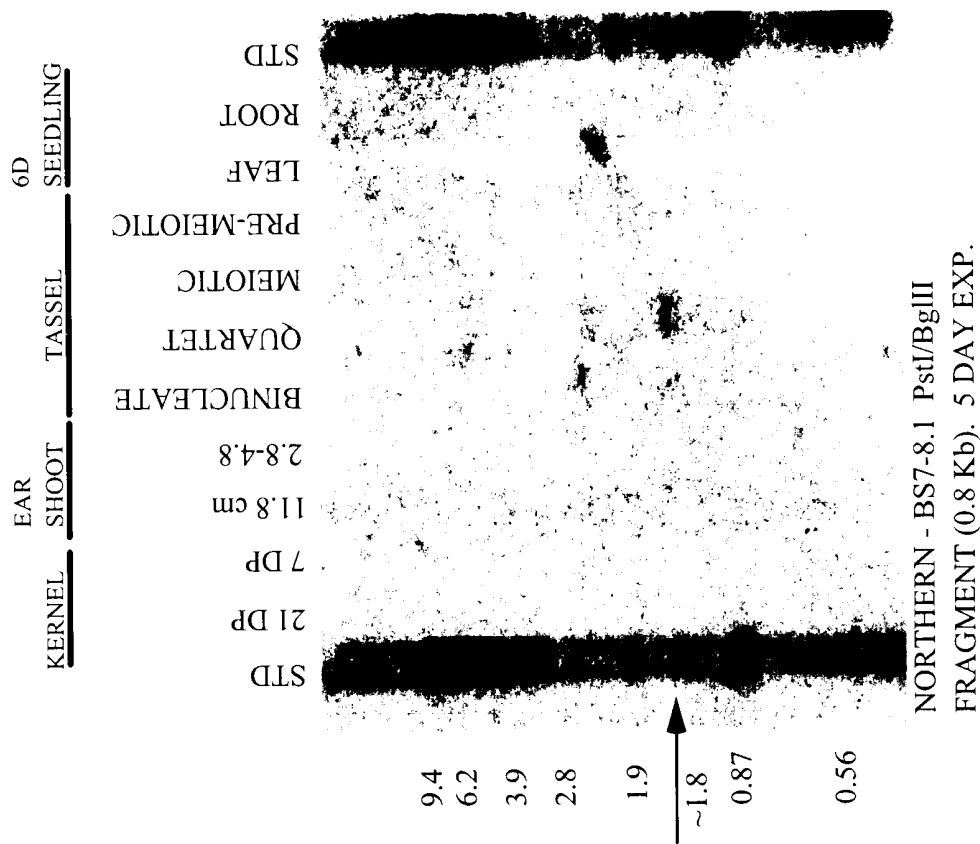


FIGURE 3

FIGURE 4

GGTGACCTCAAGCAAGGGCAAGGTATGCGTAACCGGGGCCTCAGGCTTTGTTGCCTCTTG
1 -----+-----+-----+-----+-----+-----+ 60
CCACTGGAGTTCGTTCCCGTTCCATACGCATTGGCCCCGGAGTCCGAAACAACGGAGAAC

b V T S S K G K V C V T G A S G F V A S W -

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GCTTATCAAACGGCTCCTCGAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGG
61 -----+-----+-----+-----+-----+ 120
CGAATAGTTTGCCGAGGAGCTCAGACCTATAGTACACCATCCCTGACAGTCCCTGGGTCC

b L I K R L L E S G Y H V V G T V R D P G -

AAATCACCAAAAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT
121 -----+-----+-----+-----+-----+ 180
TTTAGTGGTTTTTTGTGCGGTGGAAACCTTTAATGGACCGCGATTTCTCTCCGACGTTTA

b N H Q K T A H L W K L P G A K E R L Q I -

CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGGCCTGTGAGGG
181 -----+-----+-----+-----+-----+ 240
GCACGCTCGATTAGACAACCTTCTTCCCTCGAAGCTGTCGCGGCACTACCGGACACTCCC

b V R A N L L E E G S F D S A V M A C E G -

TGTATTCCACACTGCATCCCCGCTCTCGCTAAACCCGACTCTACTAGCAAGGAGGACAC
241 -----+-----+-----+-----+-----+ 300
ACATAAGGTGTGACGTAGGGGGCAGGAGCGATTTGGGCTGAGATGATCGTTTCCTCCTGTG

b V F H T A S P V L A K P D S T S K E D T -

GCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGATCGTGCAAGAAGAACCCCTT
301 -----+-----+-----+-----+-----+ 360
CGAGCAGGGACGCCACTTGCCATGAGACTTGCACGACTCTAGCACGTTCTTCTTGGGGAA

b L V P A V N G T L N V L R S C K K N P F -

CCTGAAAAGGGTCGTCCTTACGTCTTCGTCTGCGGTGAGGATCAGGGACGACGGTGG
361 -----+-----+-----+-----+-----+ 420
GGACTTTTCCCAGCAGGAATGCAGAAGCAGCAGACGCCACTCCTAGTCCCTGCTGCCACC

b L K R V V L T S S S S A V R I R D D G G -

CCAGTCCAGTAACATCTCGCTGGACGAAACGACATGGAGCTCCGTGCCACTCTGCGAGAA
421 -----+-----+-----+-----+-----+ 480
GGTCAGGTCAATTGTAGAGCGACCTGCTTTGCTGTACCTCGAGGCACGGTGAGACGCTCTT

b Q S S N I S L D E T T W S S V P L C E K -

FIGURE 4B

GATGCATCTATGGTATGCCCTAGCCAAGGTATTTGCAGAGAAAGCGGCGTGGGAGTTCGC
 481 -----+-----+-----+-----+-----+-----+ 540
 CTACGTAGATACCATAACGGGATCGGTTCCATAAACGTCTCTTTGCCCGCACCTCAAGCG
 b M H L W Y A L A K V F A E K A A W E F A -
 CAAGGAGAACGGCATCGACCTTGTGACTGTCTCCCGTCGTTTCGTGATCGGGCCCAGTTT
 541 -----+-----+-----+-----+-----+-----+ 600
 GTTCTCTTGCCGTAGCTGGAACACTGACAGGAGGGCAGCAAGCACTAGCCCCGGGTCAAA
 b K E N G I D L V T V L P S F V I G P S L -
 GTCCACGAGCTATGCGTTACCGCTTCAGACGTCCTAGGCCTATTCCAAGGCGACACGGC
 601 -----+-----+-----+-----+-----+-----+ 660
 CAGGGTGCTCGATACGCAATGGCGAAGTCTGCAGGATCCGGATAAGGTTCCGCTGTGCCG
 b S H E L C V T A S D V L G L F Q G D T A -
 AAGGTTTCAGCTCGTACGGAAGAATGGGGTACGTCCACATCGACGACGTTGCGAGCAGCCA
 661 -----+-----+-----+-----+-----+-----+ 720
 TTCCAAGTCGAGCATGCCTTCTTACCCCATGCAGGTGTAGCTGCTGCAACGCTCGTCGGT
 b R F S S Y G R M G Y V H I D D V A S S H -
 CATCCTGGTGTACGAGGTCCCCCAGGCCGCGGGAGGTACCTGTGCAGCTCAGTGGTGCT
 721 -----+-----+-----+-----+-----+-----+ 780
 GTAGGACCACATGCTCCAGGGGGTCCGGCGGCCCTCCATGGACACGTCGAGTCACCACGA
 b I L V Y E V P Q A A G R Y L C S S V V L -
 GGACAACGACGAGCTGGTCTCCTCGCTCGCGAAACGCTACCCGATATTCCCCATACCCCG
 781 -----+-----+-----+-----+-----+-----+ 840
 CCTGTTGCTGCTCGACCAGAGGAGCGAGCGCTTTGCGATGGGCTATAAGGGGTATGGGGC
 b D N D E L V S S L A K R Y P I F P I P R -
 GAGGCTGAACAGCCCCTACGGCAAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGG
 841 -----+-----+-----+-----+-----+-----+ 900
 CTCCGACTTGTCGGGGATGCCGTTTCGTCAGCATGGTCGACTTGTGCAGCTTCGACGTCCC
 b R L N S P Y G K Q S Y Q L N T S K L Q G -
 GCTGGGCTTCAAGTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAA
 901 -----+-----+-----+-----+-----+-----+ 960
 CGACCCGAAGTTCAAGTCTCCCAACGTCCTCTACAAGCTGCTGACGCACGTCAGCGAGTT
 b L G F K F R G V Q E M F D D C V Q S L K -
 AGACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGGTGCCTCCTGTGAA
 961 -----+-----+-----+-----+-----+-----+ 1020
 TCTGGTCCCGGTGGACGACCTCACGGGGGACACTTGACGCTACCCCAACGGAGGACACTT
 b D Q G H L L E C P L *

FIGURE 4C

CGCCCGTTTTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCAGACT
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GCGGGCAAAAAAAAAAAGAAGTTATTAAGGTGCAGTACAGTGCCACAGGAGCGCGTCTGA

GCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTACATGAATAAAATG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 CGATGACAGTCCACAGTCCCGCAGTATCGAGTGCCCGAGATGCCGATGTACTTATTTTAC

TCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAAAAAAAAAAAAAAACTCGAG
 1141 -----+-----+-----+-----+-----+-----+ 1197
 AGTGCGATCGAGCAGTAAACGAAACGGTAAATTTTTTTTTTTTTTTTTTTTGTGAGCTC

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FIGURE 5

1 GAATTCTCGT CTCGGCGGTC AACTGAACCG TAAACAGTGG AAAGTGGATA
51 CTCTTTCTCT CTCTGCAATC CGTGCCGTGG AAGCAAATGG CGCAGTCGCC
101 TACTTATCAC ACCAACTTAT CACCTAGAAA AGCGACGCGT CCTGGATCGA
151 TTGCAAATCT ACCTCCAACC AACCCAGCTT TGTATCTGCT TACTGTGATC
201 ACCAAAGTTG TGCTGATACG ATGTGCGATT ATTGCTCTTT CTTCTCTAGA
251 ATGTTCCCTGC CGATGCTTTA TAAGAGAAGG TTGGTCAGCA TCGATCTCTG
301 CCAGTGTCTA GCTGAGAAC A TGGTGACCTC AAGCAAGGGC AAGGTATGCG
351 TAACCGGGGC CTCAGGCTTT GTTGCCCTCTT GGCTTATCAA ACGGCTCCTC
401 GAGTCTGGAT ATCATGTGGT AGGGACTGTC AGGGACCCAG GTATTTGCGA
451 AATATCATT A CTATCGTATC AGTCCTCTTT ATTACATTAA TAATTCCTGA
501 TTACCAATTT TTTCTTTTTT TTTTTTGGTA ACCCACAAGG AAATCACCAA
551 AAGACAGCCC ACCTTTGGAA ATTACCTGGC GCTAAAGAGA GGCTGCAAAT
601 CGTGCGAGCT GATCTGTTGG AAGAAGGGAG CTTGACAGC GCCGTGATGG
651 CCTGTGAGGG TGTATTCCAC ACTGCATCCC CCGTCCTCGC TAAACCCGAC
701 TCTACTAGCA AGGCATGCCA TCGCCGCATA TATATATGCA TATCTGGACC
751 ATGCATCCTA CTGCAGCCTT TTCTATACGG AAGCGCGTTG CATCTACCGT
801 ACGTGAAGCT AGCTATCTAA GCTAAGCTGT TTTTCATGCA TGCATGGTGC
851 AGGAGGACAC GCTCGTCCCT GCGGTGAACG GTACTCTGAA CGTGCTGAGA
901 TCGTGCAAGA AGAACCCGTT CCTGAAAAGG GTCGTCCTTA CGTCTTCGTC
951 GTCTGCGGTG AGGATCAGGG ACGACGGTGG CCAGTCCAGT AACATCTCGC
1001 TGGACGAAAC GACATGGAGC TCCGTGCCAC TCTGCGAGAA GATGCATGTG
1051 AGATACTACT GAACAGTGTC TACTCTCTCT CTCTCTGTCA TCGATCTCAA
1101 ACCGTGATCT GAAAAACACG CATGCGCGCA CACGTTGCCG TCGTCGTCCC
1151 TTTTGTGTGTT CACCCGAAGC TATGGTATGC CCTAGCCAAG GTATTTGCAG
1201 AGAAAGCGGC GTGGGAGTTC GCCAAGGAGA ACGGCATCGA CCTTGTGACT
1251 GTCCTCCCGT CGTTCGTGAT CGGGCCCAGT TTGTCCCACG AACTATGCGT
1301 TACCGCTTCA GACGTCCTAG GCCTATTCCA AGGTATTCAT CTCAATCATT

FIGURE 5B

1351 CGTACGTGTT CTGGTTTTTCG TATGTTAAAT AGATGACTGG AAACAAGAGG

1401 TATACATATA TATACTCTCT GTTCCTCCTC CCCCCCCCCC CCCACCCCCA

1451 GGCGACACGG CAAGGTTTCAG CTCGTACGGA AGAATGGGGT ACGTCCACAT

1501 CGACGACGTT GCGAGCAGCC ACATCCTGGT GTACGAGGCC CCCCAGGCCG

1551 CCGGGAGGTA CCTGTGCAGC TCAGTGGTGC TGGACAACGA CGAGCTGGTC

1601 TCCTCGCTCG CGAAACGCTA CCCGATATTC CCCATACCCC GGAGGTCAGT

1651 CGTCGTCGCG TCGTCTGGAT GTGCGTGCCA TTTTAAGATC TCTGAACGGG

1701 AGAGCCGTGT GCATGGTCCG TTCTGCTGCA GGCTGAACAG CCCCTACGGC

1751 AAGCAGTCGT ACCAGCTGAA CACGTCGAAG CTGCAGGGGC TGGGCTTCAA

1801 GTTCAGAGGG GTGCAGGAgA TGTTCGACgA CTGCGTACAG TCGCTCAAAG

1851 ACCAGGGACA CCTGCTGGAG TGCCCCCTGT GAACTGCGAT GGGGTGCCTC

1901 CGCCTGTGAA CGCGCCGGTT GGGTTGCGTC CCGAACCCGC TGTTAATTCTG

1951 TTTTTTTTTT TCATAATAATT CCACGTCATG TCACGGTGTC CTCGCGCAgA

2001 CTGCTACTGT CAGGGCGTCA TAGCTCACGG GCTCTCCGGC TACATGAATA

2051 AAAATGTCAC GCTCGTCATT TGCTTTGCCT TTTTTTTTGG GTTCGTTCTG

2101 CGAaCTTCCG TTCGCTGTGT GTAATTGTGG CTGCCGGTCg CCTTGTCgGT

2151 GTGGCGACTG ATGATGGTGA TCGGAGGCAG GCACCGGTGT GTGCGTGCGA

2201 TCAACCGAAC GCCATGTGGC GGTTTGGATG GACGAATGGC TCCACCATCG

2251 ATCTGAGTCA TTCGGATTTT GAACCGCTGA TTTGTCCACT GGACGGCACT

2301 AGCATCAAGA TTCAGTCTCA AATCCCAAAT TCCTCAACGC AAAGCCACAA

2351 AGAGAGAATG AATGTACAGT GTTTCAAGCC ACAGCTCAcT AGcTCAAAG

2401 TAGTGAGCAT GcACACCTGT ATTTACATGC ATGCATGTAC ACCCCCACCC

2451 CCACTACTTG TACACTTTGT AAACCAACCA ACCAACCAAC CAAGCAAGCA

2501 ATCAAGCAAA CACACAGAGC AAACCGTACG TGGCTGGCGC C

Figure 6

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301 CCACTGTCTAGCTGAGAACATGGTGACCTCAAGCAAGGGCAAGGTATGCG 350
      |||
1  .....GGTGACCTCAAGCAAGGGCAAGGTATGCG 29

351 TAACCGGGGCCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 400
      |||
30 TAACCGGGGCCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 79

401 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGGTATTTGCGA 450
      |||
80 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCC..... 117

      .
      .

501 TTACCAATTTTTCTTTTTTTTTTTGGTAACCCACAAGGAAATCACCAA 550
      |||
118 .....AGGAAATCACCAA 130

551 AAGACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 600
      |||
131 AAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 180

601 CGTGCGAGCTGATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 650
      |||
181 CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 230

651 CCTGTGAGGGTGTATTCCCACTGCATCCCCCGTCCTCGCTAAACCCGAC 700
      |||
231 CCTGTGAGGGTGTATTCCCACTGCATCCCCCGTCCTCGCTAAACCCGAC 280

701 TCTACTAGCAAGGCATGCCATCGCCGCATATATATATGCATATCTGGACC 750
      |||
281 TCTACTAGCA..... 290

      .
      .

851 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 900
      |||
291 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 340

901 TCGTGCAAGAAGAACCCGTTCTGAAAAGGGTCGTCCTTACGTCTTCGTC 950
      |||
341 TCGTGCAAGAAGAACCCCTTCCTGAAAAGGGTCGTCCTTACGTCTTCGTC 390

951 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 1000
      |||
391 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 440

```

FIGURE 6B

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1001 TGGACGAAACGACATGGAGCTCCGTGCCACTCTGCGAGAAGATGCATGTG 1050
      |||
441 TGGACGAAACGACATGGAGCTCCGTGCCACTCTGCGAGAAGATGCAT... 487
      .
      .
      .
1151 TTTTGTGTTCACCCGAAGCTATGGTATGCCCTAGCCAAGGTATTTGCAG 1200
      |||
488 .....CTATGGTATGCCCTAGCCAAGGTATTTGCAG 518
      .
      .
1201 AGAAAGCGGCGTGGGAGTTCGCCAAGGAGAACGGCATCGACCTTGTGACT 1250
      |||
519 AGAAAGCGGCGTGGGAGTTCGCCAAGGAGAACGGCATCGACCTTGTGACT 568
      .
      .
1251 GTCCTCCCGTCGTTCGTGATCGGGCCAGTTTGTCCCACGAACTATGCGT 1300
      |||
569 GTCCTCCCGTCGTTCGTGATCGGGCCAGTTTGTCCCACGAGCTATGCGT 618
      .
      .
1301 TACCGCTTCAGACGTCCTAGGCCTATTCCAAGGTATTCATCTCAATCATT 1350
      |||
619 TACCGCTTCAGACGTCCTAGGCCTATTCCA..... 648
      .
      .
      .
1401 TATACATATATATACTCTCTGTTCCCTCCTCCCCCCCCCCCCACCCCCA 1450
      |
649 .....A 649
      .
      .
1451 GGCGACACGGCAAGGTTTCAGCTCGTACGGAAGAATGGGGTACGTCCACAT 1500
      |||
650 GGCGACACGGCAAGGTTTCAGCTCGTACGGAAGAATGGGGTACGTCCACAT 699
      .
      .
1501 CGACGACGTTGCGAGCAGCCACATCCTGGTGTACGAGGCCCCCAGGCCG 1550
      |||
700 CGACGACGTTGCGAGCAGCCACATCCTGGTGTACGAGGTCCCCCAGGCCG 749
      .
      .
1551 CCGGGAGGTACCTGTGCAGCTCAGTGGTGCTGGACAACGACGAGCTGGTC 1600
      |||
750 CCGGGAGGTACCTGTGCAGCTCAGTGGTGCTGGACAACGACGAGCTGGTC 799
      .
      .
1601 TCCTCGCTCGCGAAACGCTACCCGATATTCCCCATACCCCGGAGGTTCAGT 1650
      |||
800 TCCTCGCTCGCGAAACGCTACCCGATATTCCCCATACCCCGG..... 841
      .
      .
      .
1701 AGAGCCGTGTGCATGGTCCGTTCTGCTGCAGGCTGAACAGCCCCTACGGC 1750
      |||
842 .....AGGCTGAACAGCCCCTACGGC 862

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FIGURE 6C

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1751 AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 1800
      |||||||||||||||||||||||||||||||||||||||||||||||
863  AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 912
      |||||||||||||||||||||||||||||||||||||||||||||||
1801 GTTCAGAGGGGTGCAGGAgATGTTTCGACgACTGCGTACAGTCGCTCAAAG 1850
      |||||||||||||||||||||||||||||||||||||||||||||||
913  GTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAAAG 962
      |||||||||||||||||||||||||||||||||||||||||||||||
1851 ACCAGGGACACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGTGCCTC 1900
      ||||||||| ||||||||||||||||||||||||||||| |||
963  ACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGG..GGTGC 1010
      ||||||||| ||||||||||||||||||||||||||||| |||
1901 CGCCTGTGAACGCGCCGGTTGGGTTGCGTCCCGAACCCGCTGTTAATTCG 1950
      || |||||||||||||
1011 CTCCTGTGAACGCCC.....GTT 1028
      |||||||||||
1951 TTTTTTTTTTCTTCAATAATTCCACGTCATGTACGGTGTCTCGCGCagA 2000
      |||||||||||||||||||||||||||||||||||||||||||||||
1029 TTTTTTTTTTCTTCAATAATTCCACGTCATGTACGGTGTCTCGCGCAGA 1078
      |||||||||||||||||||||||||||||||||||||||||||||||
2001 CTGCTAC.....TGTCAGGGCGTCATAGCTCACGGGCTCTCCGGCTAC 2043
      ||||||| ||||||||||||||||||||||||||||| |||||||
1079 CTGCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTAC 1128
      ||||||| ||||||||||||||||||||||||||||| |||||||
2044 ATGAATAAAA...ATGTCACGCTCGTCATTTGCTTTGCCTTTTTTTTTTGG 2090
      ||||||||| || ||||||||||||||||||||||||| |||
1129 ATGAATAAAATGTCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAA 1178
      ||||||||| || ||||||||||||||||||||||||| |||
2091 GTTCGTTCTGCGAaCTTCCGTTTCGCTGTGTGTACTTGTGGCTGCCGGTCg 2140
      |
1179 AAAAAAAAAAAAACTCGAG..... 1197

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SMALL PREMEIOTIC
 LARGE PREMEIOTIC
 PREME + LEPT
 LEPT + ZYGO
 ZYGO + PACHY
 PACHY + DIPLO
 DIPLO
 MEIOSIS I
 MEIOSIS II + Q
 TELOII + Q
 QUARTET
 Q + QR
 EARLY UNI
 EU + EARLY MID
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 LATE MID + LATE UNI
 LATE UNI

Bp

— 6583
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 — 3638
 — 2604
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 — 1383
 — 953
 — 623
 — 284

DEVELOPMENTAL GENE EXPRESSION IN MICROSPORO-
 GENESIS OF THE MALE FERTILITY GENE BS92-7.
 23 HR. EXP

FIGURE 7

Figure 8

1 GAATTCTCGT CTCGGCGGTC AACTGAACCG TAAACAGTGG AAAGTGGATA
51 CTCTTTCTCT CTCTGCAATC CGTGCCGTGG AAGCAAATGG CGCAGTCGCC
101 TACTTATCAC ACCAACTTAT CACCTAGAAA AGCGACGCGT CCTGGATCGA
151 TTGCAAATCT ACCTCCAACC AACCCAGCTT TGTATCTGCT TACTGTGATC
201 ACCAAAGTTG TGCTGATACG ATGTGCGATT ATTGCTCTTT CTTCTCTAGA
251 ATGTTCTGTC CGATGCTTTA TAAGAGAAGG TTGGTCAGCA TCGATCTCTG
301 CCAGTGTCTA GCTGAGAACA **TG**

Normalized Luciferase Activity as a % of Wildtype

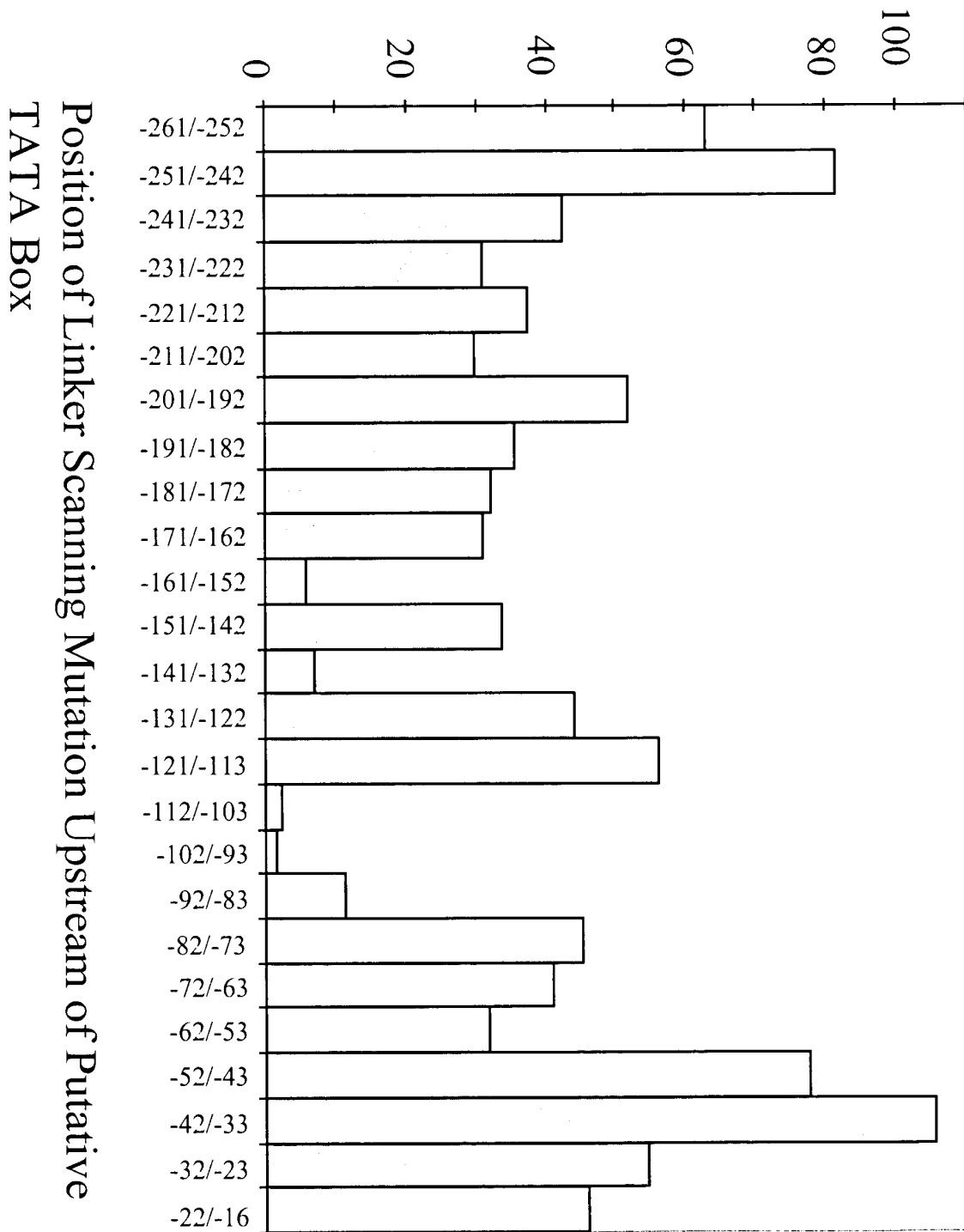


Figure 9

Figure 10

1 CGCGTCCTGG ATCGATTGCA AATCTACCTC CAACCAACCC AGCTTTGTAT
51 CTGCTTACTG TGATCACCAA AGTTGTGCTG ATACGATGTG CGATTATTGC
101 TCTTTCTTCT CTAGAATGTT CCTGCCGATG CTTTATAAGA GAAGGTTGGT
151 CAGCATCGAT CTCTGCCAGT GTCTAGCTGA GAAC**ATG**

BS7	MS45	35S	PAT
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BS7:MS45

A632

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MS45p →



Figure 11

Figure 12

5
Sorghum V T G A S G F
GTAACCGGGGCTTCAGGCT 50
Maize GTAACCGGGGCTTCAGGCT 34
10 V T G A S G F

I A S W L I K R L L E S G Y H V
Sorghum 51 TTATTGCCTCTTGGCTTATCAAACGGCTGCTCGAGTCTGGATATCATGTG 100
Maize 35 TTGTTGCCTCTTGGCTTATCAAACGGCTCCTCGAGTCTGGATATCATGTG 84
15 V A S W L I K R L L E S G Y H V

V G T V R D P G N H Q K T A H L W
Sorghum 101 GTAGGACTGTCTAGAGACCCAGGAAATCACCAAAAAACAGCACACCTTTG 150
Maize 85 GTAGGACTGTCTAGGGACCCAGGAAATCACCAAAAAACAGCCCACCTTTG 134
20 V G T V R D P G N H Q K T A H L W

K L P G A K E R L Q I V R A D L L
Sorghum 151 GAAATTACCTGGTGCCAAAGAGAGGCTGCAAATTGTGCGAGCTGATCTGT 200
Maize 135 GAAATTACCTGGCGCTAAAGAGAGGCTGCAAATCGTGCGAGCTAATCTGT 184
25 K L P G A K E R L Q I V R A N L L

E E G S F D N A V M D C D G V F
Sorghum 201 TGGAAGAAGGGAGCTTTGACAATGCTGTCTGATGGACTGTGATGGCGTCTTC 250
Maize 185 TGGAAGAAGGGAGCTTCGACAGCGCCGTGATGGCCTGTGAGGGTGTATTC 234
30 E E G S F D S A V M A C E G V F

H T A S P V L A K S D S S S K E E
Sorghum 251 CACACTGCATCCCCTGTGCTCGCTAAATCTGATTCTAGTAGCAAGGAGGA 300
Maize 235 CACACTGCATCCCCGTCTCGCTAAACCCGACTCTACTAGCAAGGAGGA 284
40 H T A S P V L A K P D S T S K E E

T L V P A V N G T L N V L R S C K
Sorghum 301 AACGCTTTGTCCAGCAGTAAACGGTACTCTGAATGTGCTAAGATCGTGCA 350
Maize 285 CACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGATCGTGCA 334
45 T L V P A V N G T L N V L R S C K

K N P F L K R V V L T S S S S A
Sorghum 351 AGAAGAACCCTTTCTGAAAAGGGTGTCTTACGTCTTCATCATCTGCA 400
Maize 335 AGAAGAACCCTTCCTGAAAAGGGTCGTCCTTACGTCTTCGTCGTCTGCG 384
50 K N P F L K R V V L T S S S S A

			V	R	I	R	D	D	D	Q	.	.	P	N	I	S	L	D	E	
5	Sorghum	401	GTGAGGATTAGGGATGATGATCAGC.....CTAATATCTCACTGGATGA	444																
	Maize	385	GTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGCTGGACGA	434																
10			V	R	I	R	D	D	G	G	Q	S	S	N	I	S	L	D	E	
			T	T	W	S	S	V	P	L	C	E	K	M	Q	L	W	Y	A	
	Sorghum	445	AACAACATGGAGCTCTGTGCCACTCTGTGAAAAGATGCAGCTATGGTATG	494																
15	Maize	435	AACGACATGGAGCTCCGTGCCACTCTGCGAAAAGATGCATCTATGGTATG	484																
			T	T	W	S	S	V	P	L	C	E	K	M	H	L	W	Y	A	
			L	A	K	V	F	A	E	K	A	A	W	E	F	A	K	E		
	Sorghum	495	CCCTAGCGAAGGTATTTGCAGAGAAAGCGGCATGGGAATTCGCCAAGGAG	544																
20																				
	Maize	485	CCCTAGCCAAGGTATTTGCAGAGAAAGCGGCGTGGGAGTTCGCCAAGGAG	534																
			L	A	K	V	F	A	E	K	A	A	W	E	F	A	K	E		
			N	N	I	D	L	V	T	V	L	P	S	F	V	I	G	P	S	
25																				
	Sorghum	545	AACAACATCGACCTTGTGACTGTCCTCCCATCATTTGTGATCGGGCCCAG	594																
	Maize	535	AACGGCATCGACCTTGTGACTGTCCTCCCGTCGTTGCGTATCGGGCCCAG	584																
			N	G	I	D	L	V	T	V	L	P	S	F	V	I	G	P	S	
30																				
			L	S	H	E	L	C	V	T	A	S	D	V	L	G	L	F	Q	
	Sorghum	595	TTTATCCCATGAACATGTGTTACCGCTTCAGATGTCTAGGCTTATTCC	644																
	Maize	585	TTTGTCCACGAGCTATGCGTTACCGCTTCAGACGTCTAGGCCTATTCC	634																
35			L	S	H	E	L	C	V	T	A	S	D	V	L	G	L	F	Q	
			G	D	T	A	R	F	S	S	Y	G	R	M	G	Y	V	H		
	Sorghum	645	AAGGTGACACGGCAAGGTTCACTTCTTACGGAAGAATGGGATACGTTTAC	694																
	Maize	635	AAGGCGACACGGCAAGGTTCACTCGTACGGAAGAATGGGGTACGTCCAC	684																
40			G	D	T	A	R	F	S	S	Y	G	R	M	G	Y	V	H		
			I	D	D	V	A	T	S											